



Mo5176new_rev.txt

<110> Bayer Aktiengesellschaft

<120> Nucleic Acids which encode
insect acetylcholine receptor subunits

<130> Le A 33 020-Foreign Countries

<140> US/09/303,232

<141> 1999-04-30

<150> DE 198 19 829.9

<151> 1998-05-04

<160> 14

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Drosophila melanogaster

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<221> CDS

<222> (372)..(2681)

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aatctcgtaa gattagttgg tattaagggc agcccatgca cacagctaaa aagggaacta 240
aaaaaacccc gacagaaca atgaaagctg cagcagctgg ataaggccga caaaaccgaa 300
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Met Lys Asn Ala Gln Leu Lys Leu Thr Glu Val Asp Asp
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gat gag ctg tgg ctg gca gta aga tta gcg cac tgc agc agc aac ttt 458
Asp Glu Leu Trp Leu Ala Val Arg Leu Ala His Cys Ser Ser Asn Phe
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agc agc agt agc agc aca aga acc acc agc agc aac cag agg cac aac 506
Ser Ser Ser Ser Ser Thr Arg Thr Thr Ser Ser Asn Gln Arg His Asn
30 35 40 45
cag caa ctc aca aca ctg caa cca agg agc tta agt aca aaa cac cac 554
Gln Gln Leu Thr Thr Leu Gln Pro Arg Ser Leu Ser Thr Lys His His
50 55 60
agc aac att gca agc gag cag cac aat agc cag caa cag gag cca gca 602
Ser Asn Ile Ala Ser Glu Gln His Asn Ser Gln Gln Gln Glu Pro Ala
65 70 75
tcg aag gac gag gat gta gcc aac cac ggt aga agc aat gac cag cag 650
Ser Lys Asp Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln
80 85 90

Mo5176new_rev.txt

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gcc gca gca gca act gct gcc ggc gat gaa gca aca acc caa caa cca Ala Ala Ala Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro 110 115 120 125	746
aca aac ata aga ctg tgt gca cgc aag cga caa cga ttg cgt cgc cga Thr Asn Ile Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg 130 135 140	794
cga aaa aga aaa cca gca acc cca aac gaa aca gat atc aag aaa caa Arg Lys Arg Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln 145 150 155	842
cag caa ctt agc atg cct ccc ttc aaa acg cgc aaa tcc acg gac acc Gln Gln Leu Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr 160 165 170	890
tac agc aca cca gca gca aca acc agc tgt ccg aca gcc acc tac atg Tyr Ser Thr Pro Ala Ala Thr Thr Ser Cys Pro Thr Ala Thr Tyr Met 175 180 185	938
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tct gct aaa gtt tgc cta gca gga tat cat gaa aag aga ctg tta cac Ser Ala Lys Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His 305 310 315	1322
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Mo5176new_rev.txt

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cgt aac gag atc tat tac aac tgc tgc ccg gaa ccc tat ata gac atc Arg Asn Glu Ile Tyr Tyr Asn Cys Cys Pro Glu Tyr Ile Asp Ile 495 500 505			1898
acc ttc gcc atc atc atc cgc cga cga aca ctg tac tat ttc ttc aac Thr Phe Ala Ile Ile Ile Arg Arg Arg Thr Leu Tyr Tyr Phe Phe Asn 510 515 520 525			1946
ctg atc ata cct tgt gta ctg att gcc tcc atg gcc ttg ctc gga ttc Leu Ile Ile Pro Cys Val Leu Ile Ala Ser Met Ala Leu Leu Gly Phe 530 535 540			1994
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Mo5176new_rev.txt

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Mo5176new_rev.txt

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 65 70 75 80
 Glu Asp Val Ala Asn His Gly Arg Ser Asn Asp Gln Gln Thr His Leu
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 Gln Gln Leu Asp Ser Ser Asn Met Leu Ser Pro Lys Thr Ala Ala Ala
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 Ala Thr Ala Ala Gly Asp Glu Ala Thr Thr Gln Gln Pro Thr Asn Ile
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 Arg Leu Cys Ala Arg Lys Arg Gln Arg Leu Arg Arg Arg Arg Lys Arg
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 Lys Pro Ala Thr Pro Asn Glu Thr Asp Ile Lys Lys Gln Gln Gln Leu
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 Ser Met Pro Pro Phe Lys Thr Arg Lys Ser Thr Asp Thr Tyr Ser Thr
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 Val Ser Leu Gln Gln Trp Gln Leu His Val Gln Gln Arg Ser Val Leu
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 Gly Ser Phe Ala Ala Gln Leu Lys Asn Ser Ser Ser Ser Ser Ser Ser
 260 265 270
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 Lys His Ser Trp Ile Phe Leu Leu Ile Tyr Leu Asn Leu Ser Ala Lys
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 Val Cys Leu Ala Gly Tyr His Glu Lys Arg Leu Leu His Asp Leu Leu
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Glu Lys Asn Gln Leu Leu Val Thr Asn Val Trp Leu Lys Leu Glu Trp
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 Asn Val Leu Asp Ile Asp Asp Asp Phe Arg His Asn Cys Arg Pro Met
 645 650 655
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 660 665 670
 Tyr Gly Gln Gly Asp Asp Gly Ser Ile Gly Pro Ile Gly Ser Thr Arg
 675 680 685

Mo5176new_rev.txt

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Tyr Glu Leu Gly Leu Ile Leu Lys Glu Ile Arg Phe Ile Thr Asp Gln
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725 730 735
Ala Ala Met Val Val Asp Arg Leu Cys Leu Ile Ile Phe Thr Met Phe
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Trp Pro Arg Gly Ala Arg Cys Gly Tyr His Glu Lys Arg Leu Leu His
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cac cta ttg gac cac tac aac gta ctg gag agg ccc gtc gtc aac gag 499
His Leu Leu Asp His Tyr Asn Val Leu Glu Arg Pro Val Val Asn Glu
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Ser Asp Pro Leu Gln Leu Ser Phe Gly Leu Thr Leu Met Gln Ile Ile
60 65 70
gac gtg gac gag aag aac cag ctt tta ata aca aac atc tgg cta aaa 595
Asp Val Asp Glu Lys Asn Gln Leu Leu Ile Thr Asn Ile Trp Leu Lys
75 80 85

Mo5176new_rev.txt

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Gly	Val	Lys	Asp	Leu	Arg	Val	Pro	Pro	His	Arg	Leu	Trp	Lys	Pro	Asp	
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gtc	ctt	atg	tac	aac	agc	gcg	gac	gaa	ggg	ttc	gac	agc	acg	tat	cca	739
Val	Leu	Met	Tyr	Asn	Ser	Ala	Asp	Glu	Gly	Phe	Asp	Ser	Thr	Tyr	Pro	
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Gly	Ile	Phe	Lys	Ser	Thr	Cys	Lys	Ile	Asp	Ile	Thr	Trp	Phe	Pro	Phe	
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Asp	Asp	Gln	Arg	Cys	Glu	Met	Lys	Phe	Gly	Ser	Trp	Thr	Tyr	Asp	Gly	
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Tyr	Gln	Leu	Asp	Leu	Gln	Leu	Gln	Asp	Glu	Gly	Gly	Gly	Asp	Ile	Ser	
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Arg	Asn	Glu	Ile	Tyr	Tyr	Asn	Cys	Cys	Pro	Glu	Pro	Tyr	Ile	Asp	Ile	
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Thr	Phe	Ala	Val	Val	Ile	Arg	Arg	Lys	Thr	Leu	Tyr	Tyr	Phe	Phe	Asn	
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ctg	atc	gtg	ccc	tgc	gtg	ctc	atc	gcc	tcc	atg	gct	cta	ttg	ggg	ttc	1123
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Thr	Leu	Pro	Pro	Asp	Ser	Gly	Glu	Lys	Leu	Ser	Leu	Gly	Val	Thr	Ile	
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tta	ctg	tcg	ttg	acg	gtg	ttc	ctc	aac	atg	gtg	gcg	gag	acg	atg	cca	1219
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gcg	acg	tcg	gac	gcc	gtg	ccc	ttg	ctc	ggc	acc	tac	ttc	aac	tgc	atc	1267
Ala	Thr	Ser	Asp	Ala	Val	Pro	Leu	Leu	Gly	Thr	Tyr	Phe	Asn	Cys	Ile	
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Met	Phe	Met	Val	Ala	Ser	Ser	Val	Val	Ser	Thr	Ile	Leu	Ile	Leu	Asn	
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tac	cac	cac	cgg	cac	gca	gac	act	cac	gaa	atg	agt	gat	tgg	att	cgt	1363
Tyr	His	His	Arg	His	Ala	Asp	Thr	His	Glu	Met	Ser	Asp	Trp	Ile	Arg	

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cccctgtaga cataagttac cgctgactgc caaccctgta cgttcaacaa ataactgccc 2022			
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Mo5176new_rev.txt

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<213> *Heliothis virescens*

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Mo5176new_rev.txt

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 Gly Ser Trp Thr Tyr Asp Gly Tyr Gln Leu Asp Leu Gln Leu Gln Asp
 180 185 190
 Glu Gly Gly Gly Asp Ile Ser Ser Phe Val Thr Asn Gly Glu Trp Glu
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 Pro Glu Pro Tyr Ile Asp Ile Thr Phe Ala Val Val Ile Arg Arg Lys
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 305 310 315 320
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 Val Leu Arg Met Ser Arg Pro Gly Ser Ala Thr Thr Pro Pro Pro Ala
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 Arg Val Pro Pro Pro Pro Asp Leu Glu Leu Arg Glu Arg Ser Ser Lys
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Mo5176new_rev.txt

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 105 110 115
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 Page 12

Mo5176new_rev.txt

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Mo5176new_rev.txt

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Mo5176new_rev.txt

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Lys Glu Arg Ser Ser Lys Ser Leu Leu Ala Asn Val Leu Asp Ile Asp
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